LISTING OF CLAIMS

1. *(currently amended)*: A screening method for identifying, in a library of potential binding domains (PBDs) from a biological source, a polypeptide binding domain or domains that bind to a target epitope or family of target epitopes, comprising:

(a) providing a cDNA library from ~~said~~ a selected biological source that encodes said library of PBDs as a T7 phage display library wherein the PBDs are displayed on the outer surface of ~~said~~ T7 phages as fusion proteins with ~~an outer surface protein (OSP)~~ a capsid protein encoded by gene 10A or 10B of said T7 phages;

(b) contacting said phage display library with an ~~bindable~~ array of predetermined target peptides as target epitopes or a family ~~families~~ of target peptides as target epitopes, which family comprises peptides corresponding to a protein fragment, a protein domain or a complete protein, and for which target epitopes a binding partner from said biological source is sought, said contacting being conducted under conditions where any of said PBDs binds to ~~said~~ its target epitope;

(c) removing unbound T7 phages from said array of target epitopes, so that phages remaining bound are a first sublibrary enriched for PBD-displaying phages;

(d) eluting bound T7 phage from said array of target epitopes ; and

(e) determining the DNA sequences encoding the PBDs from said first sublibrary of eluted T7 phage, thereby identifying the PBDs displayed on said eluted phage by their predicted amino acid sequences encoded by said DNA sequence.

2. **CANCEL**

3. **CANCEL**

4. *(currently amended)*: The method of claim 1 [[3]], comprising, after said eluting step (d) and before said determining step (e), the step of:

(f) subjecting said eluted phage to at least one additional round of the contacting step (b) and the removing step ~~of steps (b) and~~ (c) to further enrich phage displaying said PBDs that bind to set predetermined target epitope or epitopes, thereby obtaining a second sublibrary and subsequent sublibraries.

5. *(currently amended)*: The method of claim 4 wherein step (f) is repeated more than once prior to said determining step (e), wherein after each repeat, ~~obtaining~~ a new subsequent sublibrary is obtained.

6. **CANCEL**

7. *(currently amended)*: The method of claim 1, 4 or 5 [[6]] wherein said outer surface protein capsid protein encoded by gene 10B of phage T7.

8. *(original*: The method of claim 7 wherein in said display library, said PBDs are expressed in a copy number of about 5-10 PBDs per phage particle.

9. *(original*: The method of claim 7 wherein, in said phage display library, said PBDs are expressed in high copy number of 415 PBDs per page particle.

10. *(original*: The method of claim 7 wherein in said phage display library, said PBDs are expressed in an intermediate copy number of about 100 to about 150 PBDs per page particle.

11. *(currently amended)*: The method of ~~any of~~ claim[[s]]] 1, 4 or 5, wherein said determining step (e) is performed by plating said eluted phage on a lawn of *E. coli*, permitting them to multiply and form plaques, and sequencing the DNA of the phages of any given plaque to obtain the sequence of the cDNA insert that encodes said PBD and thereby, the amino acid sequence of said PBD.

12. **CANCEL**

13. *(withdrawn/currently amended):* The method of claim 1 [[12]], wherein said family of target peptide epitopes comprises a progressive series of overlapping peptides of about 10 to 15 amino acids, each of which peptides lacks ***n*** amino-terminal amino acid residues of its predecessor peptide in the series and has at least ***n*** additional amino acids added to its carboxy-terminus, wherein ***n*** is an integer between 1 and 5, and wherein said series of overlapping peptides corresponds to (i) a region of said protein of up to about 100 amino acids, or (ii) said complete protein.

14. *(currently amended)*: The method of claim 1, 4 or 5 [[12]] wherein said target peptides or family of target peptides are synthesized in parallel on polyethylene pins mounted on blocks which are compatible with standard microplate arrays of 96 wells or multiples thereof.

15. *(original/withdrawn)*: The method of claim 13 wherein said target peptides are synthesized in parallel on polyethylene pins mounted on blocks which are compatible with standard microplate arrays of 96 wells or multiples thereof.

16. *(currently amended)*: The method of claim 14, wherein the target peptides or family of target peptides are covalently attached to the pins so that said, after said eluting of said bound phages, the blocks are reused for one or more additional screening assays.

17. *(original/withdrawn):* The method of claim 15, wherein the target peptides are covalently attached to the pins so that said, after said eluting of said bound phages, the blocks are reused for one or more additional screening assays.

18. (*original withdrawn*): The method of claim 17, wherein the target peptides are in a cleavable form, allowing recovery of said peptides.

19. *(currently amended)*: The method of ~~any of~~ claim[[s]] 1 [[-]], 4 or 5, wherein said cDNA library is produced from mRNA molecules of said biological source by random priming wherein each cDNA molecule that is reverse transcribed from said mRNA molecules is between about 50 and about 5000 bp in length, the cDNA molecules are gel purified and directionally cloned into said T7 phage DNA resulting in fused DNA, and said fused DNA is packaged into phage *in vitro*.

20. *(original*: The method of claim 19 wherein the cDNA molecule is between about 50 and about 1000 bp in length.

21. *(original*: The method of claim 20 wherein the cDNA molecule is between about 50 and 500 bp in length.

22. *(original*: The method of claim 21 wherein the cDNA molecule is between about 100 and 200 bp in length.

26. *(currently amended)*: The method of any of claims 1, 4 or -5 wherein the biological source is selected from the group consisting of developing chick neural retina, cultured neonatal rat Schwann cells, and myelinating sciatic nerves of 15-25 day old rats.

30. *(currently amended)*: The method of any of claims 1, 4 or-5, wherein

(a) the phage display library displays PBDs of synaptotagmin (SytI) and the target epitopes are peptides of synaptotagmin (Syt IV); or

(b) the phage display library displays PBDs of SytIV and the target epitopes are peptides of Syt I.